



WO 02/098916

16 / 28

GAAP1 GAP-1 CODING SEQUENCE

- SEQ ID NO: 38 and 39

GAAP1 ATGGCATTAAGGTAATCAAAGTCCACAGTAGTGAATTCAAGCAATAAGTGCCCTCTGAAATTACAGTG 70

PROII ATGCCATTAGGTAATCAAAGTCCACAGTAGTGAATTCAAGCAATAAGTGCCCTCTGAAATTACAGTG 70

GAAP1 AGCAACATAAAGAAAATCCCTTAATCAAAGTGAACCAAGAAGAAATTAAATTTTGATGGCTTAATAA 140

PROII AGCAAGATAAAGAAAATCCCTTAATCAAAGTGAACCAAGAAGAAATTAAATTTTGATGGCTTAATAA 140

↓ ↓
GAAP1 GTCAAAATGAAGAGTAGTAAATGCTTCAGGCCACCGGAGTCAGCAAAATCATTGGAAGATGTCGAATA 210

PROII GTCAAAATGAAGAGTAGTAAATGCTTCAGGCCACCGGAGTCAGGAAGATCATTGGAAGATGTCGAATA 210

GAAP1 CGTTGTAAGAAAACCTAGCTGTAAAGAACACATACGAACCCATACGATGTCGCGGGCTAACACATGCA 280

PROII CGTTGTAAGAAAACCTAGCTGTAAAGAACACATACGAACCCATACGATGTCGCGGGCTAACACATGCA 280

GAAP1 CTTACTGTAACCTCTCTTAAAGCTTAACGAAATCTGCACAAACACATGTCAGTCAGCTCAAGCACATGCA 350

PROII CTTACTGTAACCTCTCTTAAAGCTTAACGAAATCTGCACAAACACATGTCAGTCAGCTCAAGCACATGCA 350

↓
GAAP1 GAAATCTCTGGATTAGGCATCTCAGTAGCTTAAGCTGCAACGGATACAGAAGATCAGTCAAAAA 420

PROII GAAATCTCTGGATTAGGCATCTCAGTAGCTTAAGCTGCAACGGATACAGAAGATCAGTCAAAAA 420

GAAP1 CAGACATTCAGMTCAGGCACTCTGGATAGCTCTGAAATCTGAAATCTGATGCGGCGATGAGGATCACATG 490

GAAP1 CAGACATTCAGMTCAGGCACTCTGGATAGCTCTGAAATCTGAAATCTGATGCGGCGATGAGGATCACATG 490

GAAP1 AAAATGAGACGGATCTGAGGCAACGCGAACCTGAAATCTGCTTCAGGACACACCTCTAGTCACAGCTAG 560

PROII AAAATGAGACGGATCTGAGGCAACGCGAACCTGAAATCTGCTTCAGGACACACCTCTAGTCACAGCTAG 560

GAAP1 CCGGCAACCTCTCTCTAGAAGTACGCTTCAGGACCGCTCTGAGTACGAGGGATGTCAGCTCAAC 630

PROII CCGGCAACCTCTCTAGAAGTACGCTTCAGGACCGCTCTGAGTACGAGGGATGTCAGCTCAAC 630

GAAP1 GATTGCTTCTCTGGGTACACAOGGGCTCAATGCGCTCTGCGAGGGCGCTGCTCAOCAGAAATGACIG 700

PROII GATTGCTTCTCTGGGTACACAOGGGCTCAATGCGCTCTGCGAGGGCGCTGCTCAOCAGAAATGACIG 700

GAAP1 TCTGAGGACACCCACACTCTGACTCTACAGGAGCTCTGCTCTGCGAGGGCGCTGCTCAOCAGAAATGACIG 770

PROII TCTGAGGACACCCACACTCTGACTCTACAGGAGCTCTGCTCTGCGAGGGCGCTGCTCAOCAGAAATGACIG 770

GAAP1 GAGAGATGAAACGACACATTCGGCTCTGAGTACGCTTCAGGACCGCTGCTCAOCAGAAATGACIG 840

FIGURE 14A (a)

REPLACEMENT SHEET

WO 02/098916

PCT/EP02/07064

17 / 28

PROII GAGAGATGAAAGACACAMTCCGTCGTGACACTTCAGGTTCCCGTCGTCATGTCGGAC 840
 GAAP1 TACCCCTGAGCAGAAGAAATTCTGAGAACCTCTATGGAGAAAACCTGTTGCTTAACAGAGGCGAT 910
 PROII TACCCCTGAGCAGAAGAAATTCTGAGAACCTCTATGGAGAAAACCTGTTGCTTAACAGAGGCGAT 910
 GAAP1 CACCTGTAAGACTTCCCTGAGGTCAGGACAGGCCCCAGCAGGAGGGATGCTTCGAGGC 980
 PROII CACCTGTAAGACTTCCCTGAGGTCAGGACAGGCCCCAGCAGGAGGGATGCTTCGAGGC 980
 GAAP1 CTCAACACATCTGACCTCTCAAGAACAGAACAGCAGCAAAATRACTCTACAGGCGACTCTGCGCTCT 1050
 PROII CTCAACACATCTGACCTCTCAAGAACAGAACAGCAGCAAAATRACTCTACAGGCGACTCTGCGCTCT 1050
 GAAP1 CCOCACACTCATTTGTTAGCCACCTTCTTGCATTOOCAGCAGCAATGGCGCGCTTAAATGG 1120
 PROII CCOCACACTCATTTGTTAGCCACCTTCTTGCATTOOCAGCAGCAATGGCGCGCTTAAATGG 1120
 GAAP1 TTCCAGTTCccccccATOCATGTTGCTTCTCTCTACATCTACAGGTTGCGCTTCAGCTGG 1190
 PROII TTCCAGTTCccccccATOCATGTTGCTTCTCTCTACATCTACAGGTTGCGCTTCAGCTGG 1190
 GAAP1 ACCAGTGACCTCAACGTTCCGTCAGGTCGTCACGACTTTGGGACTCTACAGGAGGGTC 1260
 PROII ACCAGTGACCTCAACGTTCCGTCAGGTCGTCACGACTTTGGGACTCTACAGGAGGGTC 1260
 GAAP1 ACAGAAGTGCTGGACTACAAACCTCTGGACTGGCTGAATTAAAGCAGTCGCTGGCTATCTCA 1330
 PROII ACAGAAGTGCTGGACTACAAACCTCTGGACTGGCTGAATTAAAGCAGTCGCTGGCTATCTCA 1330
 GAAP1 TGGCCAAATGGCGAGGCGCTTCAGAACCTCTGGACTGGCTGAATTAAAGCAGTCGCTGGCTATCTCA 1400
 PROII TGGCCAAATGGCGAGGCGCTTCAGAACCTCTGGACTGGCTGAATTAAAGCAGTCGCTGGCTATCTCA 1400
 GAAP1 CATGGAAACCGTCATAATGAGGCTTGGCTTACAAATGGCGCTTCAGAACCTCTGGACTGGCT 1470
 PROII CATGGAAACCGTCATAATGAGGCTTGGCTTACAAATGGCGCTTCAGAACCTCTGGACTGGCT 1470
 GAAP1 CCTGCTGAATGCTGGCTCCGGTCTGACTCTGCAAACCCCTCATCACAAAGCAGGGGGGGGCTGAGG 1540
 PROII CCTGCTGAATGCTGGCTCCGGTCTGACTCTGCAAACCCCTCATCACAAAGCAGGGGGGGGCTGAGG 1540
 GAAP1 CACACATTGAGGCTCCGACTCTGAAACATGCCATTGGCCACCTTAATCCCTCTGCTTCAGCTGC 1610
 PROII CACACATTGAGGCTCCGACTCTGAAACATGCCATTGGCCACCTTAATCCCTCTGCTTCAGCTGC 1610
 GAAP1 CGTTCATGACAGGCGCTCCGACTCTGAAAGCAAAAGCATGGCTGCGCTGACACCCGAGG 1680

FIGURE 14A (b)

REPLACEMENT SHEET

WO 02/098916

PCT/EP02/07064

18 / 28

PRDII CGTTGATGCCAACAGGCGTCCGAAATGGCGTCCCCAGGAAAGCCTGCGACGACAAACCGCG 1680

GAAP1 ACTTCCTGTAGCCAGGCCAACCAGGTAGCAGGAGGAGGTCTCTCTAGGGGTTACGTCAGTCCAGGGG 1750

PROII ACTTCCTGTAGCCAGGCCAACCAGGTAGCAGGAGGAGGTCTCTCTAGGGGTTACGTCAGTCCAGGGG 1750

GAAP1 AAAATGCAAAAAAAAGTTCTGAATCCAOCTGODDCTCGAATGACCTGCAAGCTTGATGGCGTGATA 1820

PROII AAAATGCAAAAAAAAGTTCTGAATCCAOCTGODDCTCGAATGACCTGCAAGCTTGATGGCGTGATA 1820

GAAP1 AATGGCACACAGAGAGCTGGCTGGCAAATCACTGAAACCCAAGCTGAACTCACCTCTCGATACGGGC 1890

PROII AATGGCACACAGAGAGCTGGCTGGCTGGCAAATCACTGAAACCCAAGCTGAACTCACCTCTCGATACGGGC 1890

GAAP1 CAACCAAGGTGCAACTCACAAACCTCTGGCTGAACTCACATCTGAGCTTTCGAAACCCCTCAGGCCAGC 1960

PROII CAACCAAGGTGCAACTCACAAACCTCTGGCTGAACTCACATCTGAGCTTTCGAAACCCCTCAGGCCAGC 1960

GAAP1 AGACTCTCTCTCGACAGCAAGCTTGGCGAACAGACTACGGGAAACCTGCGACCTGCGACCT 2030

PROII AGACTCTCTCTCGACAGCAAGCTTGGCGAACAGACTACGGGAAACCTGCGACCTGCGACCT 2030

GAAP1 CAGCGAAGTCAGCAAGCAGTCAGAGGACGCGGCTGAGATGCAACCTGATG 2084

PROII CAGCGAAGTCAGCAAGCAGTCAGAGGACGCGGCTGAGATGCAACCTGATG 2084

FIGURE 14A (c)

REPLACEMENT SHEET

WO 02/098916

PCT/EP02/07064

1 GRAP-1 CODING SEQUENCE

19 / 28

SEQ ID NO: 44

ATGGGGCAGAAGTTCAAAAAAGAGA

GCATTAGGTAACTAAAAGTOCACAGTACGTCATTCAGCAATTAAGTGGCTCTGAAATTACAGTG

GAAP1 ACCRAAGATAAGAAATTCCITAATCAAAGTGACACAGAACATTAATTTCATGCCATATTA

GAAP1 GTCAAATGAAAGAGTATGTAATGCGGGAGGGAAATTCATTTGAAAGAATGTCATA

GAAP1 CGTTCGAAAGAAACCTAACCCNCTAAAGAAACACATACGAACCCATCAGTGCGGCGGCGACACTGCA

GAAP1 CTTAACGTAACTTCCTTAACTAAAGGAATCTGACAAACACATGAGTOCAAGCACATACCAA

GAAP1 GAATGCGGATTAGGCGTCTAGTAAAGTAAAGCAACACGTTACGAGATCAAGATGAGATGAA

GAAP1 CAGACGTTACGTTACGCGTCTGGATATGCTTGAACATCTGATGGCGCGATGAGATCACAA

GAAP1 AAAATGAGACCGATATGAGGACAGCCAGCTGAATCAGTGTGCGCACACCGCTCAGTCAGCG

GAAP1 CGCGCAGCCCTTCACTCTAGAGTACCCCTTACGGCGCTGAGTACTGACCGGCTCAGGTCAAC

GAAP1 GATTCCTTTCTGGGCTACACAOGGCCCGAACTGCTCTGCGGAGGGCGCTGACCCAGATGCTAC

GAAP1 TCCCTGGCACAGCACCTCTGACTACATAGGAGACACCTCTCGGGGAGCGCGCGCGCGCTGC

GAAP1 GCGCGATGAAACCCACACAAATCGCTCTGAGACACTTGGTCCCCCGTCACATGTCGTCGAGAC

FIGURE 14B (a)

REPLACEMENT SHEET

WO 02/098916

PCT/EP02/07064

20 / 28

GAAP1 TACGCTGAGTCAGAAGAAATTCTGAGAAGTTCTATGGCAGGAAAGCCTGTGCATAACAGAGCCAT

GAAP1 CMTCTGTAAGACTTCTCTCTCCCTGGACCTGAGCAAGGCCCCCAACGACCAACGGCGTCAGTCAGTGCC

GAAP1 CTCACCACATCTGACCTCTAAGAACAGGAGCAAATACTCTAACGGCAACTCTGGCTTGCTCT

GAAP1 CCCACACATCTGTTAGGACCTCTCTCTGGCTTGGCATTOCCAGGAGCAATGGAGAACCTTAAATTCG

GAAP1 TTOAGTTCGGGGATOCATGGTACCTGGTACCTGGCTCACATACTAACGGTTGGCTTCAAGCTTC

GAAP1 ACCAGTGCACTCAOGATOCTGCTGCTGAGGCTCTCAACACTTGGTACTCAAGGAATCCGTC

GAAP1 ACAGAAGTGCTGGCACTAACAAACCTGCTGGAGTGGCTGAATTAGGAGTGTGTCATGTATCCAA

GAAP1 TCGCCAAATCGGCTGCAAGGCTTCAGACCTAAGTAACCGCTTCAGACTCTGGTACTCAAGCTAGTTAG

GAAP1 CATGGAAACCTCATATGTAACCTTAACAAATACAAATATGGCCCCAACACTCCATTCACAGGACTG

GAAP1 GCTCTGAAAGCTGCTGGTACTCCGGCTCTGCTGCAAAACCTTCATCACAAAGGAGCCCCCTGAG

GAAP1 CACACATTGAGGTCCTCAAGATCTTGAACATAGCAATTGGCAACCTTAATCCCTTACGTCAGTCAGTAGC

GAAP1 CGTGTGATGCAAGGGAGCTGGCAATGCGAGCTGCGAAAGCAAGCATGCGAGACACAACCCAAAGCAG
FIGURE 14B (b)

REPLACEMENT SHEET

WO 02/098916

PCT/EP02/07064

21 / 28

PRO111 CGTTGATGCACGCCAGCTCCAGAAATGCCAGCTTCCAAAGCAAAGCATGGTGACACAAACCGAAGCAG

GAAP1 ACTTCCTGTAGCCAGGCCAACCAAGGTGACCAAGGAACGAGTCTCTCTAGGGGTAACCTACAGTCCAGCCCG

GAAP1 AAATGCAAAAAAAACTTCCTGAACTACCCGCCCTCCAGGTGACCAAGGCTTGATGCCCTGAGTAA

GAAP1 AAAGGACACAGACAAGGTGCCCCTGGCAAAATCACCTGAGGCCAACGCTGAACTCACTTOCATACAGGCC

GAAP1 CAAACCAGGGTCCACGTACAACCTCTGCTGAGCCACATTCTGAGTTTTCACAAAGGCCCTGAGGCCAGC

GAAP1 AGACTCTCTCTTCAAGTCAAGCAGGTGACCAAGGCCAACCTCTGCTGAGTTTTCACAAAGGCCCTGAGGCCAGC

GAAP1 CAAACCAGGTGAGCAAGGATGTCAGGAGACGCCCTCTGAAACCAACCTGAGTC

FIGURE 14B (c)

REPLACEMENT SHEET

WO 02/098916

PCT/EP02/07064

GAAP-2 coding seq

22 / 28

SEQ ID NO: 45

1 ATGGGGCAGA AGTTCAAAA AAAGAAATCT TACAGGCTGG TGTTAAAGGA
TACCCCGTCT TCAAAGTTT TTTCTTACA ATGCCGACC ACAATTCT

51 ACTTCGGAAT CCCTTAAAGA GAGCATTAGG TAATCAAAAG TCCACAGTAG
TGAAGCCTTA GGGAAATTCT CTCGTAATCC ATTAGTTTC AGGTGTCA

101 TTGAATTCAAG CAATAAAAGAT GCCTCTGAAA TTAAACAGTGA GCAAGATAAA
AACTTAAGTC GTTATTCTA CGGAGACTT AATGTCACT CGTTCTATT

151 GAAAATTCT TAATCAAAAG TGAACCAAGA AGAATTAAJA TATTGATGG
CTTTTAAGGA ATTAGTTTC ACTTGGTCT TCTTAATTAT ATAAACTACC

201 AGGATATAAG TCAAATGAAG AGTATGTATA TATCCGAGGC AGGGGAAGAG
TCCTATATTC AGTTTACTTC TCATACATAT ATAGGCTCCG TCCCCCTCTC

251 GAAAATACAT TTGTGAAGAA TGTGGAATAC GTTGTAAGAA ACCTAGCATG
CTTTATGTA AACACTTCTT ACACCTTATG CAACATTCTT TGGATCGTAC

301 TTAAAGAAC ACATACGAAC CCATACAGAT GTCCGCCCT ACCACTGCAC
AATTTCTTG TGTATGCTTG GGTATGCTA CAGGCGGGGA TGGTGACGTG

351 TTACTGTAAC TTCTCCCTTA AGACTAAAGG AAATCTGACA AAACACATGA
AATGACATTG AAGAGGAAAT TCTGATTTC TTTAGACTGT TTTGTGTACT

401 AGTCCAAGGC ACATAGCAAG AAATGTGTGG ATTTAGGCAT CTCAGTAGGT
TCAGGTTCCG TGTATGCTTC TTTACACACC TAAATCCGIA GAGTCATCCA

451 TTAATAGATG AACAGGATAC AGAAGAATCA GATGAAAAAC AGAGATTCA
AATTATCTAC TTGTCCTATG TCTTCTTAGT CTACTTTTG TCTCTAAGTC

501 TTATGAGCGA TCTGGATATG ATCTGAAAGA ATCTGATGGC CCAGATGAGG
AATACTCGCT AGACCTATAC TAGAACTTCT TAGACTACCG GGTCTACTCC

551 ATGACAATGA AAATGAAGAC GATGATGAGG ACAGCCAGGC TGAATCAGTC
TACTGTTACT TTTACTTCTG CTACTACTCC TGTGGTCCG ACTTAGTCAG

601 CTGTCAGCCA CACCCCTCACT CACAGCTAGC CCGCAGCACC TTCCATCTAG
GACAGTCGGT GTGGGAGTCA GTGTCGATCG GGCGTCGTGG AAGGTAGATC

651 AAGTAGCCTT CAGGACCCCTG TGAGTACTGA CGAGGATGTC AGGATCACCG
TTCATCGGAA GTCCGGGAC ACTCATGACT GCTCTACAG TCCTAGTGGC

701 ATTGCTTTTC TGGGGTACAC ACGGACCCCA TGGACGTTCT GCCCAGGGCG
TAACGAAAAG ACCCCATGTG TGCTGGGT ACCTGCAAGA CGGGTCCCCC

751 CTGCTCACCA GAATGACTGT CCTGAGCACA GCACAGTCTG ACTACAATAG
GACGAGTGGT CTTACTGACA GGACTCGTGT CGTGTCAAGAC TGATGTTATC

801 GAAGACACTC TCTCCGGGGA AGGCCAGGCA GCGTGTGCG AGAGATGAAA
CTTCTGTGAG AGAGGCCCCCT TCCGGTCCGT CGCACGACG TCTCTACTTT

851 ACGACACAAAT TCCGTCGTA GACACTCCA GGTCCCCGTG TCAATCAGATG
TGCTGTGTTA AGGCAGACAT CTGTGAAGGT CCAGGGCA AGTAGTCTAC

901 TCTGTGGACT ACCCTGAGTC AGAACAAATT CTGAGAAGTT CTATGGCAGG
AGACACCTGA TGGGACTCAG TCTTCTTAA GACTCTCAA GATACCGTCC

FIGURE 14C (a)

REPLACEMENT SHEET

WO 02/098916

PCT/EP02/07064

23 / 28

951 AAAAGCTGTT GCTATAACAC AGAGCCCATC ATCTGTAAGA CTTCCCTCCTG
TTTCGACAA CGATATTGTG TCTCGGGTAG TAGACATTCT GAAGGAGGAC

1001 CTGCAGCTGA GCACAGCCCC CAGACAGCAG CGGGGATGCC TTCTGTGGCC
GACCTCGACT CGTGTGGGG GTCTGTGTC GCCCCTACCG AAGACACCGG

1051 TCACCACATC CTGACCCCTCA AGAACAGAAAG CNGCAAATTA CTCTACAGCC
AGTGGTGTAG GACTGGGAGT TCTTGTCTTC GTCTGTTATT GAGATGTCGG

1101 GACTCCAGGC TTGCCTCTC CCCACACTCA TTTGTTTAGC CACCTTCCTT
CTGAGGTCCG AACGGAAGAG GGGTGTGAGT AAACAAATCG GTGGAAGGAA

1151 TGCATTCCC GCAGCAATCG AGGACACCTT ATAATATGCT TCCAGTTGGG
ACGTAAGGGT CGTCGTTAGC TCCTGTGGAA TATTATACCA AGGTCAACCC

1201 GGGATCCATG TGGTACCTGC TGGCCTCACA TACTCCACGT TTGTGCCCT
CCCTAGGTAC ACCATGGAGC ACCGGAGTGT ATGAGGTGCA AACACGGGA

1251 TCAGGCTGGA CCAGTGCAGC TCACGATCCC TGCTGTCACT GTCTGTTACA
AGTCCGACCT GGTACGTG AGTGCTAGGG AGCACAGTCA CAGCAAGTGT

1301 GAACTTTGGG TACTCATAGG AATACGGTCA CAGAAGTGTG TGGCACTACA
CTTGAAACCC ATGAGTATCC TTATGCCAGT GTCTTCACAG ACCGTGATGT

1351 AACCCCTGCTG GAGTGGCTGA ATTAAGCACT GTTGTGCCAT GTATTCCAT
TTGGGACGAC CTCACCGACT TAATTGTC CAACACGGTA CATAAGGATA

1401 CGGCCAAATC CGCGTGCAG GCCTTCAGAA CCTAAGTAC CCAGGCTTGC
GCCGGTTAG GCGCACGGTC CGGAAGTCTT GGATTCACTGG GGTCCGAACG

1451 AGTCACTCCC CTCGTTAACG ATGGAAACCG TCAATATTGT AGGCCTAGCC
TCAGTGAGGG GAGCAATTG TACCTTGGC AGTTATAACA TCCGGATCGG

1501 AATACAAATA TGGCCCCACA AGTCATCCA CCAGGACTG CTCTGAATGC
TTATGTTAT ACCGGGGTGT TCAGGTAGGT GGTCTGAC GAGACTTACG

1551 TGTCGGACTG CAGGTCTGA CTGCAAACCC TTCAATCACA AGCAGCCCCG
ACAGCCTGAC GTCCAAGACT GACGTTGGG AACTAGTGT TCGTCGGGGC

1601 CCCCTCAGGC ACACATTCCA GGTCTCCAGA TCTTGAACA AGCATTGCC
GGGGAGTCCG TGTGTAAGGT CCAGAGGTCT AGAACATTGTA TCGTAACGGG

1651 ACCTTAATCC CCTCAGTCAG TCAAGTAGCC GTTGATGCAC AGGGAGCTCC
TGGATTAGG GGAGTCAGTC AGTTCATCGG CAACTACGTG TCCCTCGAGG

1701 AGAAATGCCA GCTTCCAAA GCAAAGCATG CGAGACACAA CCCAAGCAGA
TCTTACGGT CGAAGGGTTT CGTTCTGTC GCTCTGTGTT GGGTTCGTCT

1751 CTTCTGTAGC CAGCGCAAAC CAGGTCAAGCA GGACCGAGTC TCCTCAGGGG
GAAGACATCG GTCGCGTTG GTCCAGTCGT CCTGGCTCAG AGGAGTCCCC

1801 TTACCTACAG TCCAGCGGGAA AAATGCAAA AAAGTTCTGA ATCCACCTGC
AATGGAAIGTC AGGTGCCCCCT TTTACGTTT TTTCAAGAC1 TAGGTGGACG

1851 CCCTGCAGGT GACCAGTGCAGA GGCTTGATGG CCTGAGTAAP ATGGACACAG
GGGACGTCCA CTGGTACGTT CCGAACTACCC GGACTCATTI TACCTGTGTC

FIGURE 14C (b)

REPLACEMENT SHEET

WO 02/098916

PCT/EP02/07064

24 / 28

1901 AGAAGGCTGC CTCGGCAAAT CACGTGAAGC CCAAGCCTGA ACTCACTTCC
TCTTCCGACG GAGCCGTTA GTGCACTTCG GGTCGGACT TGAGTGAAGG

1951 ATACAGGGCC AACCAGCGTC CACGTACAA CCTCTGCTGA AGGCACATTC
TATGTCCCAG TTGGTCGCAG GTGCAGTGTT GGAGACGACT TCCGTGTAAG

2001 TGAAGTTTT ACAAAACCCCT CAGGCCAGCA GACTCTCTCT CCAGACAGAC
ACTTCAAAAA TGTTTGGGA GTCCGGTCGTT CTGAGAGASA GGTCTGTCTG

2051 AGGTTCCCAG GCCCACAGGA CTACCCCGGA GCCAGCCCAC TGTGCACTTC
TCCAAGGGTC CGGGTGTCT GATGGCGCCT CCGTCGGGTG ACACGTGAAG

2101 AGCGACGTGA GCAGCGATGA TGACGAGGAC AGGCTTGTA TAGAACCTG
TCGCTGCACT CGTCGCTACT ACTGCTCCTG TCCGAACACT ATCGTTGGAC

2151 A
T

FIGURE 14C (c)

REPLACEMENT SHEET

WO 02/098916

PCT/EP02/07064

25 / 28

SEQ ID NO: 40 and 41

2 GRAP-1 POLYPEPTIDE

>GRAP-1

GRAP1 MALGNQKSTIVVEFSNKDASEINSEODRENSLIKSBRPRKIFDGGYKSNERYVVRGRGCKVTCRPGI 70
 PROLI MALGNQKSTIVVEFSNKDASEINSEODRENSLIKSBRPRKIFDGGYKSNERYVVRGRGCKVTCRPGI 70

GRAP1 RCRKPSMLKKHIRTIDVVPYHCTCNFSPTRKGM/LKEMSKAHSRKCVILGVSVGLIDRQDITRSOK 140
 PROLI RCRKPSMLKKHIRTIDVVPYHCTCNFSPTRKGM/LKEMSKAHSRKCVILGVSVGLIDRQDITRSOK 140

GRAP1 QFPSYERSGVDLLESDGPDEDENENKQDDEDSQAESVLATPSVIAASPHLPSRSSLQDPVSIIDRVIT 210
 PROLI QFPSYERSGVDLLESDGPDEDENENKQDDEDSQAESVLATPSVIAASPHLPSRSSLQDPVSIIDRVIT 210

GRAP1 DCPSGVHIDPMQVLRAALLTRMIVLSTAQSDINRKILSPCKARQRAAQNUTIPSVDISRSPCHQMVD 280
 PROLI DCPSGVHIDPMQVLRAALLTRMIVLSTAQSDINRKILSPCKARQRAAQNUTIPSVDISRSPCHQMVD 280

GRAP1 YPKEEETILRSMAGRAVALTQSPSSVLPFFAAEHSPQTAAGMPVAASPHPDQPKQOITLOPTPGLPS 350
 PROLI YPKEEETILRSMAGRAVALTQSPSSVLPFFAAEHSPQTAAGMPVAASPHPDQPKQOITLOPTPGLPS 350

GRAP1 PTHILFSLPLHSQOSETPYNMVPVGGIRVVERGLITYSTIFVPLAQEVOLTLPAVSWERDLGIRNIV 420
 PROLI PTHILFSLPLHSQOSETPYNMVPVGGIRVVERGLITYSTIFVPLAQEVOLTLPAVSWERDLGIRNIV 420

GRAP1 TEVSGITINPAGVAEELSSWPCIPICQJIRVPGQLNLSTEGLOSPLSLSMETIVGLANIDMAPQVHPPGL 490
 PROLI TEVSGITINPAGVAEELSSWPCIPICQJIRVPGQLNLSTEGLOSPLSLSMETIVGLANIDMAPQVHPPGL 490

GRAP1 ACNAVGLOWLTANPSSQSSPAPQAHPLQINTIALPTLIPSVSQAVADQGAPMEMASQSKACETOPQ 560
 PROLI ALNAVGLOWLTANPSSQSSPAPQAHPLQINTIALPTLIPSVSQAVADQGAPMEMASQSKACETOPQ 560

GRAP1 TSVASANQVRIEESPOQLPTVORENARKVLINEPAPACDHARLDLSRMOTKAASANVKPKPELTSIQC 630
 PROLI TSVASANQVRIEESPOQLPTVORENARKVLINEPAPACDHARLDLSRMOTKAASANVKPKPELTSIQC 630

GRAP1 QFASITSOPLKAKSEVFIRPSGQOILSPDROVERPTALERPROFTVHPSDVSDDDDDRQVIAT 694
 PROLI QFASITSOPLKAKSEVFIRPSGQOILSPDROVPRPTGLERPROFTVHPSDVSDDDDDRQVIAT 694

FIGURE 15 A

REPLACEMENT SHEET

WO 02/098916

PCT/EP02/07064

26 / 28

SEQ ID NO: 46

2 GAAP-1 POLYPEPTIDE

>GAAP-1

M GOKPQKCR ALGNDKSTIVWEESNKDASKINS EQLDKENSLIKSEPRRIKIDEGYRSNEEVVVRGRGGKYICCEBOGI

GAAP1 RCKKPSMLKKHHRKHTDVRPVHCTYONFSFKTKGNLTKHMKSIAHSKKCVDLGVSGLIIDSQUTSDEK

GAAP1 QRFSYERSGYDLEESDGETEDDNENEEDDSQAESVLSATPSVTASPOHLPSRSSTLQDFVSTDDEOVRIT

GAAP1 DCFSGVEIDPMVLPRALLTRMVLSTIAQSDYKNTLSPGKAPQRAARDENDTIPSVDISRSPCHOMSVD

GAAP1 YPESHEKILRSSMAGKAVAITQSPSSVRLPPAAAERSPOTAGMPVASPHPDPOBOKOORTLQFTPGLPS

GAAP1 FTHILFSHLPLHSQQQSPTPYNMVFGGIRVVPAGLTYSTFVPLQAGPVQUTIPAVSVWHRYLGHRRNIV

GAAP1 TEVSGMTNFAGVAELSSWPCLPIGQIRVPGQNLSTPGQSLPSLSMETAVNLVGLANTNMAPQVHPPL

GAAP1 A-NAVGLQVLTANPSSQSSPAPOAHIGLQILNTALPILIPSVSQAVDAQGAFEMPASQSKACETOQKQ

GAAP1 TSVASANQVKTESPOGLPTIVORENAKKVLNPAPAGDARLUGLSKMDTEKAASANEVKPKPEUTSIQG

GAAP1 QPASTSQPLIKAHSEVFTRPSQOQLSPDROVPRPTALPRROPTVHFSDVSSDDEDRLVIAAT

FIGURE 15 B

REPLACEMENT SHEET

WO 02/098916

PCT/EP02/07064

27 / 28

6 AAP-2

SEQ ID NO: 47

1 MGQKFQKKKS YRLVILKELRN PLKRALGNQK STVVVEFSNKD ASEINNSEQDK

51 ENSLIKSEPR RIKIFDGGYK SNEEYVYIRG RGRGKYICEE CGIRCKKPSM

101 LKKHIRHTD VRPYHCTYCN FSFKTKGNLT KRMKSKAHSK KCVDLGISVG

151 LIDEQDTEES DEKQRFSYER SGYDLEESDG PDEDDNENDD DDEDSSQAESV

201 LSATPSVTAS PQHLPSRSSL QDPVSTDDEV RITDCFSGVH TDPMMDVLPR

251 LLTRMTVLST AQSDYNRKTL SPGKARQRAA RDENDTIPSV DTSPSPCHQM

301 SVDYPESEEI LRSSMAGKAV AITQSPSSVR LPPAAAERSP QTAAGMPSVA

351 SPHPDPQEQQ QQITLQOPTPG LPSPHTHLFS HLPLHSQQQS RTPYNMVPVG

401 GIHVVPAGLT YSTFVPLQAG PVQLTIPAVS VVHRTLGTHR NTVTEVSGTT

451 NPAGVAELSS VVPCIPIGQI RVPGLQNLST PGLQSLPSLS METVNIVGLA

501 NTNMAPQVHP PGLALNAVGL QVLTANPSSQ SSPAPQAHIP GLQILNIALP

551 TLIPSVSQVA VDAQGAPEMP ASQSKACETQ PKOTSVASAN QVSRTESPQG

601 LPTVQRENAK KVLNPPAPAG DHARLDGLSK MDTEKAASAN HVKPKPELTS

651 IQQQPASTSQ PLLKAHSEVF TKPSGQQTLS PDRQVPRPTG LPRRQPTVHF

701 SDVSSDDDED RLVIAT

FIGURE 15 C